Numerical simulation of a spatial – temporal model of epidemic distribution

Numerical simulation of a spatial – temporal model of epidemic distribution

T.S. Timofeeva[1] **, I.Farago, and E.L.Kim**

[1]North-Eastern Federal University, 48 Kulakovskogo str., Yakutsk 677000, Russia

E-mail: timofeevatc@mail.ru

Abstract. The problem of epidemiological situation forecasting is considered. The system of differential equations that describes the development of the epidemic process with regard to spatial dependence, proposed in works I.Farago and based on the Kermak-MacKendrick model. The paper presents the results of numerical calculations for different mathematical models of the spread of infectious diseases with different levels of detail.

1. Introduction

Infectious diseases have always been and still remain the most dangerous for the human body due to their ability to involve a large number of healthy people in a short period of time. There are many especially dangerous viruses, which are evaluated as a very effective means of waging biological warfare. Bioterrorism is an extremely serious threat to humanity.

Natural as well as social processes influence the rise and course of epidemic. Infectious diseases are among the diseases that significantly affect the indicators of health and life expectancy of the population. Therefore, it is very important to understand the mechanism of the epidemic and try to prevent its spread using such effective and affordable means as vaccination.

A timely and adequate prognosis is a prerequisite for planning the structure, scale, and timing of measures aimed at preventing epidemic and outbreak of diseases, as well as at reducing their negative consequences.

To model the rise, development and extinction of epidemic, systems of differential equations are often used, which, depending on the type of a model, determine the dynamics of the transition of individuals from one group to another. The most well-known is the SIR model, proposed by Kermack and McKendrick [1], as well as its generalizations [2, 3, 4]. The Kermack and McKendrick model is registered as a Cauchy problem for a system of ordinary differential equations:

$$\begin{aligned} \frac{dS}{dt} &= -aSI, \qquad t \in (0,T], \\ \frac{dI}{dt} &= aSI - bI, \qquad t \in (0,T], \\ \frac{dR}{dt} &= bI, \qquad t \in (0,T], \end{aligned} \tag{1}$$

where $S(t)$ is a number of people predisposed to a disease, $I(t)$ are infected individuals who are able to spread the disease, and $R(t)$ are individuals who had been infected and left the number

of infected as a result of recovery or death. The disease coefficient a depends on the population density and the characteristic signs of the disease, and the recovery rate b depends inversely on the duration of the disease.

Using this model, we can calculate how many people should be immunized before the epidemic wave reaches a certain region, and we can stop the spread of the disease. Mathematical models can be used in the analysis and prediction of indicators of infectious diseases rate. Their use as a prediction tool is limited to modeling the spread of a single-type infection and its consequences. Modeling permits to predict the epidemiological situation, analyze the spatial spread of diseases, explore the mechanisms causing epidemic, develop programs to control and eradicate diseases, and analyze various preventive means. When building a model, it is necessary to take into account a number of limitations and assumptions about the nature of the disease and the structure of the population under consideration.

A number of models have been designed to detail the SIR and make possible their practical use. For example, in research [3], a SIR modification with dynamic parameters is used to predict the spread of HIV.

2. Spatial model of the disease distribution

Point models in their original form are not able to simulate the spatial movement of the disease. For example, they show the number of infected people depending on time, but do not give any information about their location. The location of infectious diseases and relations between neighboring countries have also played an important role in cases of an epidemic outbreak. Therefore, while modeling epidemics, it is necessary to take into account the spatial characteristics of the distribution of infection and the influence of geographical factors. Then the system of equations includes the mechanisms of movement of individuals between territories with a given intensity. As a result, we obtain the following one-dimensional initial-boundary problem for the system of partial differential equations:

$$\begin{aligned} \frac{\partial S}{\partial t} &= -S\Big(\delta I + \varphi \frac{\partial^2 I}{\partial x^2}\Big), \quad x \in (0, L), \quad t \in (0, T], \\ \frac{\partial I}{\partial t} &= S\Big(\delta I + \varphi \frac{\partial^2 I}{\partial x^2}\Big) - bI, \quad x \in (0, L), \quad t \in (0, T], \\ \frac{\partial R}{\partial t} &= bI, \quad x \in (0, L), \quad t \in (0, T] \end{aligned} \tag{2}$$

with following initial and boundary conditions

$$\begin{aligned} S(x,0) = S_0(x), \quad I(x,0) = I_0(x), \quad R(x,0) = R_0(x), \quad x \in [0, L], \\ S(x,t) = S_0(x), \quad I(x,t) = I_0(x), \quad R(x,t) = R_0(x), \quad x = 0, L, \quad t \in (0, T], \end{aligned} \tag{3}$$

where $S = S(x,t)$, $I = I(x,t)$, $R = R(x,t)$ depend on the spatial position and density of the relevant parts of the population. The initial - boundary problem 2 - 3 is called the sSIR spatial model.

For the numerical solution of the mathematical model 2 - 3, the finite difference method was used. A symmetric difference type of the Crank-Nicholson scheme was used, which provides a second order of accuracy with respect to $0(\tau^2 + h^2)$, where $\tau = T/M$ is the time grid step, $h = L/N$ is the spatial grid step. Since the difference scheme is implicit and nonlinear, the Picard iterations are used for numerical solution.

We present results of the numerical solution for following model parameters:

$$L = 1, \quad T = 1240, \quad \delta = 0.01, \quad b = 0.03, \quad \varphi = \delta^3/12, \quad N = 100, \quad M = 620.$$

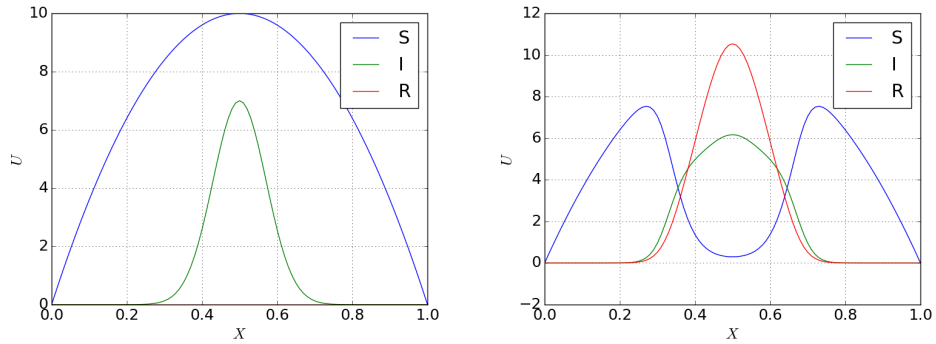

Figure 1: Initial contition (left) and numerical solution for $t = 40$ (right)

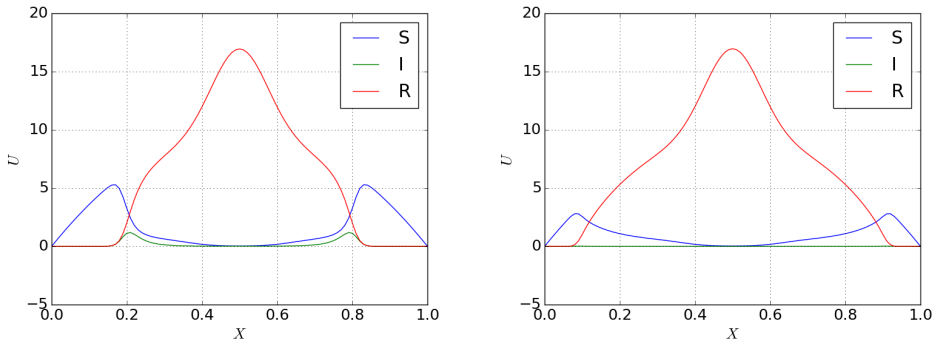

Figure 2: Results for $t = 240$ (left) and $t = 1240$ (right)

The mathematical model describes a situation when an infected individual infects more strongly than the uninfected, who are located at a distance less than δ. Initial conditions are given in the form:

$$S_0(x) = -40x(L-x), \quad I_0 = 7e^{100(x-L/2)^2}, \quad R_0 = 0, \quad x \in [0, L].$$

Fig. 1 - 2 show the distribution of S, I, R at the initial moment and at different moments in time. They are in good agreement with the results of the work [1], although it contains the calculations using explicit and linearized difference schemes. The number of iterations steadily decreases from 7 to 2 with increasing time. It should be noted that the exit from the iterative process was carried out when the following condition was fulfilled

$$\|R^{k+1} - R^k\| < 10^{-6}.$$

From the counting results it can be seen that over time the number of predisposed $S(x,t)$ to the disease decreases, the number of the infected $I(x,t)$, i.e. disease distribution also decreases, the number of the recovered$R(x,t)$ increases.

Next, we present the results of the numerical solution of a two-dimensional model problem with the following parameters:

$$L_1 = L_2 = 1, \quad T = 1240, \quad \delta = 0.01, \quad b = 0.03, \quad \varphi = \delta^3/12, \quad N = 100, \quad M = 620.$$

Initial conditions are given in the form:

$$S_0(x,y) = x(L-x)y(L-y)/(L/2)^4, \quad I_0(x,y) = 7e^{100[(x-L/2)^2+(y-L/2)^2}, \quad R_0(x,y) = 0, \quad x \in [0, L].$$

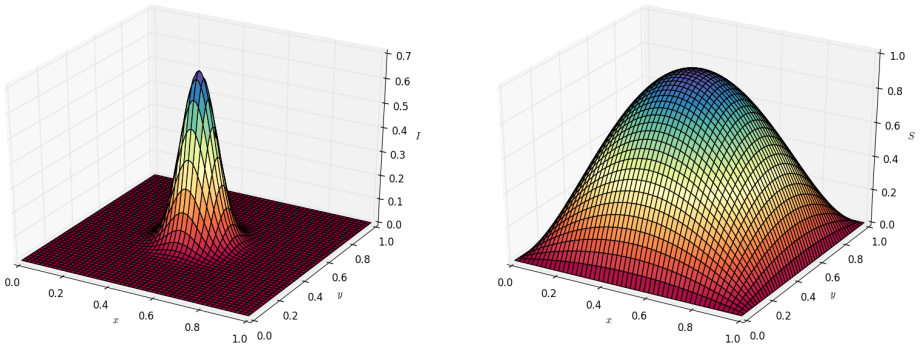

Figure 3: Initial condition for $I_0(x, y)$ (left) and $S_0(x, y)$ (right)

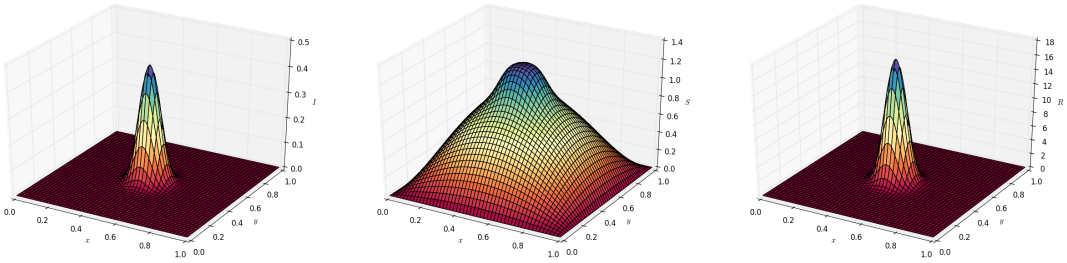

Figure 4: Numerical results for $I(x, y, T)$, $I(x, y, T)$ and $R(x, y, T)$ (from left to right)

The counting results of the two-dimensional model reproduce the counting results of one-dimensional model. The number of iterations on the time layers with time increase monotonously decreases from 14 to 2. Initial conditions and numerical results for $I(x, y, T)$, $I(x, y, T)$ and $R(x, y, T)$ are presented in Figs. 3 and 4.

3. Spatial model of the disease distribution with regard to fertility and mortality

When modeling "slow" infectious diseases characterized by long incubation and infectious periods (tuberculosis, HIV / AIDS), and when studying long-term circulation "rapid" infections, characterized by short incubation and infectious periods (measles, flu), demographic processes are taken into account. Therefore, it is necessary to take into account fertility and mortality in the mathematical models. In the classical spatial SIR model, we also included the case of the inflow of newborns into the class of susceptible individuals and the outflow of the dead from the group of susceptible, infected and insensitive individuals. Then the generalized model is recorded as follows:

$$\begin{aligned} \frac{\partial S}{\partial t} &= -S\Big(\delta I + \varphi \frac{\partial^2 I}{\partial x^2}\Big) + \mu(I + R), \quad x \in (0, L), \quad t \in (0, T], \\ \frac{\partial I}{\partial t} &= S\Big(\delta I + \varphi \frac{\partial^2 I}{\partial x^2}\Big) - (b + \mu)I, \quad x \in (0, L), \quad t \in (0, T], \\ \frac{\partial R}{\partial t} &= bI - \mu R, \quad x \in (0, L), \quad t \in (0, T], \end{aligned} \tag{4}$$

where b is a coefficient interpreted as the speed of recovery, μ is the death rate / fertility rate.

This mathematical model is supplemented by the initial and boundary conditions (3). For numerical solution of the mathematical model (4) - (3), we construct approximation using the finite difference method. Crank - Nicholson scheme was used for approximation by time and

provide a second order of accuracy with respect to $0(\tau^2 + h^2)$. Since the discretization of the system of equations (4) represent a system of nonlinear equations, we used the Picard iterations for solution of the nonlinear discrete problem.

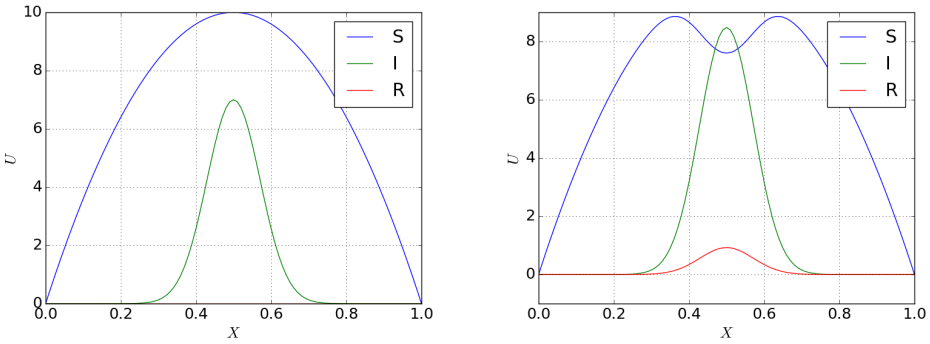

Figure 5: Initital condition (left) and numerical solution for $t = 40$ (right)

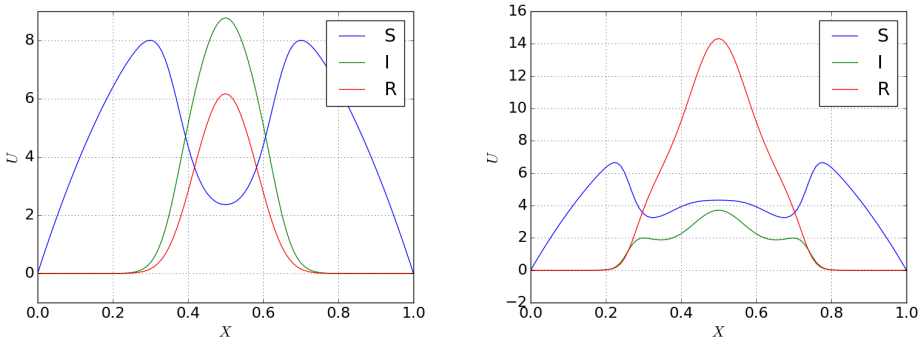

Figure 6: Numerical results for $t = 240$ (left) and $t = 1240$ (right)

We present the results for the constructed numerical implementation of the difference schemes. In the calculations for the spatial model of the disease distribution (4) - (3), we set:

$$L = 1, \quad T = 1860, \quad \delta = 0.01, \quad b = 0.03, \quad \varphi = \delta^3/12, \quad \mu = 0.00001, \quad N = 100, \quad M = 620.$$

We set the same initial conditions as in the previous model:

$$S_0(x) = -40x(L - x), \quad I_0 = 7e^{100(x-L/2)^2}, \quad R_0 = 0, \quad x \in [0, L].$$

Fig. 5 - 6 show the graphs of the distribution of S, I and R at the initial time and for different time of simulations. They are in good agreement with the results of the work of Professor I. Farago, although it carried out calculations using explicit and linearized difference schemes. The number of iterations monotonously decreases from 9 to 2 as time increases. It should be noted that the exit from the iteration process was carried out under the condition

$$\|R^{k+1} - R^k\| < 10^{-6}.$$

From the above results it can be seen that the accounting of mortality / fertility significantly slows down the healing process.

4. Conclusion

A mathematical spatial - temporal model of the infectious disease distribution was studied numerically. The model is an initial boundary value problem for the system of three partial differential equations for densities of healthy, infected and recovered populations. With the help of a numerical simulations, various situations of the epidemic in space were investigated.

References

[1] Kermack, W.O., McKendrick, A.G.: A contribution to the mathematical theory of epidemics // Proc. R. Soc. A Math. Phys. Eng. Sci. 1927. 115(772), 700–721.
[2] I.Farago, R.Horvath. On some qualitatively adequate discrete space-time models of epidemic propagation. J. of Computational and applied mathematics. 2016. 293, 45-54.
[3] I.Farago, R.Horvath. Qualitative properties of the finite difference solution of a space-time epidemic propagation model. Annales Univ. Sci. Budapest., Sect. Comp. 2016. 45, 157-168.
[4] I. Farago, R. Horvath, Qualitative properties of some discrete models of disease propagation, J. of Computational and applied mathematics. 2018. 340, 486–500.